

# SEQUENCE LISTING

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 The Regents of the University of California  
 The Government of the United States of America  
 as represented by the Secretary of the  
 Department of Health and Human Services

<120> Mammalian Sweet Taste Receptors

<130> 02307E-120110US

<140> US 09/927,315  
 <141> 2001-08-10

<150> US 60/302,898  
 <151> 2001-07-03

<160> 25

<170> PatentIn Ver. 2.1

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 <211> 840  
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 <213> Rattus sp.

<220>  
 <223> rat T1R1 sweet taste receptor

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 Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His Gly Asp  
 35 40 45  
 Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp Arg Pro  
 50 55 60  
 Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met Arg Phe  
 65 70 75 80  
 Thr Val Glu Glu Ile Asn Asn Ser Ser Ala Leu Leu Pro Asn Ile Thr  
 85 90 95  
 Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ala Asn Val Tyr  
 100 105 110  
 Ala Thr Leu Arg Val Leu Ala Leu Gln Gly Pro Arg His Ile Glu Ile  
 115 120 125

Gln Lys Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Phe Ile Gly  
 130 135 140  
 Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu Gly Pro  
 145 150 155 160  
 Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Val Leu Ser  
 165 170 175  
 Ala Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Arg  
 180 185 190  
 His Gln Val Glu Val Met Val Gln Leu Leu Gln Ser Phe Gly Trp Val  
 195 200 205  
 Trp Ile Ser Leu Ile Gly Ser Tyr Gly Asp Tyr Gly Gln Leu Gly Val  
 210 215 220  
 Gln Ala Leu Glu Glu Leu Ala Val Pro Arg Gly Ile Cys Val Ala Phe  
 225 230 235 240  
 Lys Asp Ile Val Pro Phe Ser Ala Arg Val Gly Asp Pro Arg Met Gln  
 245 250 255  
 Ser Met Met Gln His Leu Ala Gln Ala Arg Thr Thr Val Val Val Val  
 260 265 270  
 Phe Ser Asn Arg His Leu Ala Arg Val Phe Phe Arg Ser Val Val Leu  
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 Ala Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Asp Trp Ala Ile  
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 Ser Thr Tyr Ile Thr Ser Val Thr Gly Ile Gln Gly Ile Gly Thr Val  
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 340 345 350  
 Glu Gly Ser Trp Cys Ser Thr Asn Gln Leu Cys Arg Glu Cys His Thr  
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 Phe Thr Thr Arg Asn Met Pro Thr Leu Gly Ala Phe Ser Met Ser Ala  
 370 375 380  
 Ala Tyr Arg Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly Leu His  
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 Gln Leu Leu Gly Cys Thr Ser Glu Ile Cys Ser Arg Gly Pro Val Tyr  
 405 410 415  
 Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu Leu His  
 420 425 430  
 Glu Asn Thr Val Ala Phe Asp Asp Asn Gly Asp Thr Leu Gly Tyr Tyr  
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Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe Glu Ile  
 450 455 460  
 Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn Lys Thr  
 465 470 475 480  
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 515 520 525  
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 530 535 540  
 Pro Lys Glu Ser Thr Thr Cys Phe Pro Arg Thr Val Glu Phe Leu Ala  
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 Trp His Glu Pro Ile Ser Leu Val Leu Ile Ala Ala Asn Thr Leu Leu  
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 Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr Arg Thr Trp  
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 Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu Cys Thr  
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 <212> PRT  
 <213> Mus musculus

<220>  
 <223> mouse T1R1 sweet taste receptor

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 Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp  
 50 55 60  
 Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met  
 65 70 75 80  
 Arg Phe Thr Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn  
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 Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn  
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 Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu  
 115 120 125  
 Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu  
 130 135 140  
 Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu  
 145 150 155 160  
 Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile  
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 Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser  
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Asp Lys Tyr Gln Val Glu Val Ile Val Arg Leu Leu Gln Ser Phe Gly  
 195 200 205  
 Trp Val Trp Ile Ser Leu Val Gly Ser Tyr Gly Asp Tyr Gly Gln Leu  
 210 215 220  
 Gly Val Gln Ala Leu Glu Glu Leu Ala Thr Pro Arg Gly Ile Cys Val  
 225 230 235 240  
 Ala Phe Lys Asp Val Val Pro Leu Ser Ala Gln Ala Gly Asp Pro Arg  
 245 250 255  
 Met Gln Arg Met Met Leu Arg Leu Ala Arg Ala Arg Thr Thr Val Val  
 260 265 270  
 Val Val Phe Ser Asn Arg His Leu Ala Gly Val Phe Phe Arg Ser Val  
 275 280 285  
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 Ala Ile Ser Thr Tyr Ile Thr Asn Val Pro Gly Ile Gln Gly Ile Gly  
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 Thr Val Leu Gly Val Ala Ile Gln Gln Arg Gln Val Pro Gly Leu Lys  
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 Glu Phe Glu Glu Ser Tyr Val Gln Ala Val Met Gly Ala Pro Arg Thr  
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 Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys  
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 His Ala Phe Thr Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met  
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 Leu His Gln Leu Leu Gly Cys Thr Ser Gly Thr Cys Ala Arg Gly Pro  
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 Val Tyr Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu  
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 Glu Val Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn  
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 610 615 620  
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 Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln  
 645 650 655  
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 Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr  
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 Leu Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile  
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Gln Asp Tyr Thr Arg Arg Cys Gly Thr Thr  
 835 840

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 <213> Homo sapiens

<220>  
 <223> human T1R1 sweet taste receptor

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 35 40 45  
 Val Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile  
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 Glu Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val  
 65 70 75 80  
 Ile Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu  
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 Ser Pro Phe Leu Val His Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu  
 100 105 110  
 Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp  
 115 120 125  
 Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp  
 130 135 140  
 Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly  
 145 150 155 160  
 Val Gln Ala Leu Glu Asn Gln Ala Leu Val Arg Gly Ile Cys Ile Ala  
 165 170 175  
 Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met  
 180 185 190  
 Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val  
 195 200 205  
 Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val  
 210 215 220  
 Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala  
 225 230 235 240  
 Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met  
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Tyr	Asn	Ile	Ile	Ala	Trp	Asp	Trp	Asn	Gly	Pro	Lys	Trp	Thr	Phe	Thr	
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Thr	Lys	Ile	Gln	Trp	His	Gly	Lys	Asn	His	Gln	Val	Pro	Lys	Ser	Val	
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Ala	Leu	Arg	Glu	His	Thr	Ser	Trp	Val	Leu	Leu	Ala	Ala	Asn	Thr	Leu	
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Asp	Thr	Pro	Val	Val	Arg	Ser	Ala	Gly	Gly	Arg	Leu	Cys	Phe	Leu	Met	
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Glu	Pro	Thr	Arg	Pro	Ala	Cys	Leu	Leu	Arg	Gln	Ala	Leu	Phe	Ala	Leu	
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Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu  
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 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala  
 595 600 605  
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala  
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 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu  
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 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys  
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 Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly  
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 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu  
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 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu  
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<210> 4

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<212> DNA

<213> Rattus sp.

<220>

<223> rat T1R1 sweet taste receptor

<400> 4

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<212> DNA

<213> Mus musculus

<220>

<223> mouse T1R1 sweet taste receptor

<400> 5

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<210> 6

<211> 2333

<212> DNA

<213> Homo sapiens

<220>

<223> human T1R1 sweet taste receptor

<400> 6

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<210> 7

<211> 843

<212> PRT

<213> Rattus sp.

<220>

<223> rat T1R2 sweet taste receptor

<400> 7

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Met Gly Pro Gln Ala Arg Thr Leu Cys Leu Leu Ser Leu Leu Leu His
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Val Leu Pro Lys Pro Gly Lys Leu Val Glu Asn Ser Asp Phe His Leu
      20              25              30

Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
  35              40              45

Lys Ser Ile Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
  50              55              60

Phe Thr Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
  65              70              75              80

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
      85              90              95

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile His
  100              105              110

Pro Gly Leu Tyr Phe Leu Ala Gln Asp Asp Asp Leu Leu Pro Ile Leu
  115              120              125

Lys Asp Tyr Ser Gln Tyr Met Pro His Val Val Ala Val Ile Gly Pro
  130              135              140

Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser His Phe
  145              150              155              160

Leu Ile Pro Gln Ile Thr Tyr Ser Ala Ile Ser Asp Lys Leu Arg Asp
      165              170              175

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Lys Arg His Phe Pro Ser Met Leu Arg Thr Val Pro Ser Ala Thr His  
 180 185 190  
 His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp  
 195 200 205  
 Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His  
 210 215 220  
 Leu Leu Ser Gln Arg Leu Thr Lys Thr Ser Asp Ile Cys Ile Ala Phe  
 225 230 235 240  
 Gln Glu Val Leu Pro Ile Pro Glu Ser Ser Gln Val Met Arg Ser Glu  
 245 250 255  
 Glu Gln Arg Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser  
 260 265 270  
 Ala Arg Val Val Val Val Phe Ser Pro Glu Leu Ser Leu Tyr Ser Phe  
 275 280 285  
 Phe His Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala  
 290 295 300  
 Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu  
 305 310 315 320  
 Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile  
 325 330 335  
 Pro Gly Phe Ser Gln Phe Arg Val Arg Arg Asp Lys Pro Gly Tyr Pro  
 340 345 350  
 Val Pro Asn Thr Thr Asn Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp  
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 Ala Cys Leu Asn Thr Thr Lys Ser Phe Asn Asn Ile Leu Ile Leu Ser  
 370 375 380  
 Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala  
 385 390 395 400  
 His Ala Leu His Arg Leu Leu Gly Cys Asn Arg Val Arg Cys Thr Lys  
 405 410 415  
 Gln Lys Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn  
 420 425 430  
 Phe Thr Leu Leu Gly Asn Arg Leu Phe Phe Asp Gln Gln Gly Asp Met  
 435 440 445  
 Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Asp Leu Ser Gln Asn  
 450 455 460  
 Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Ser Lys Arg Leu Thr  
 465 470 475 480  
 Tyr Ile Asn Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Val  
 485 490 495

Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Ser Val  
 500 505 510  
 Gly Leu His Pro Cys Cys Phe Glu Cys Leu Asp Cys Met Pro Gly Thr  
 515 520 525  
 Tyr Leu Asn Arg Ser Ala Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly  
 530 535 540  
 Ser Met Trp Ser Tyr Lys Asn Asp Ile Thr Cys Phe Gln Arg Arg Pro  
 545 550 555 560  
 Thr Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Ala Ile Leu  
 565 570 575  
 Ala Ala Leu Gly Phe Phe Ser Thr Leu Ala Ile Leu Phe Ile Phe Trp  
 580 585 590  
 Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys  
 595 600 605  
 Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val  
 610 615 620  
 Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe  
 625 630 635 640  
 Phe Thr Val Cys Phe Ser Ile Cys Leu Ser Cys Ile Thr Val Arg Ser  
 645 650 655  
 Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala  
 660 665 670  
 Tyr Ser Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe  
 675 680 685  
 Ile Thr Ala Ile Lys Val Ala Leu Val Val Gly Asn Met Leu Ala Thr  
 690 695 700  
 Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Met  
 705 710 715 720  
 Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr  
 725 730 735  
 Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Met  
 740 745 750  
 Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu  
 755 760 765  
 Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met  
 770 775 780  
 Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr  
 785 790 795 800  
 Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys  
 805 810 815

Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn  
820 825 830

Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser  
835 840

<210> 8

<211> 843

<212> PRT

<213> Mus musculus

<220>

<223> mouse T1R2 sweet taste receptor

<400> 8

Met Gly Pro Gln Ala Arg Thr Leu His Leu Leu Phe Leu Leu Leu His  
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Ala Leu Pro Lys Pro Val Met Leu Val Gly Asn Ser Asp Phe His Leu  
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Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val  
35 40 45

Lys Ser Val Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu  
50 55 60

Tyr Asn Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe  
65 70 75 80

Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu  
85 90 95

Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile Gln  
100 105 110

Pro Gly Leu Tyr Phe Leu Ser Gln Ile Asp Asp Phe Leu Pro Ile Leu  
115 120 125

Lys Asp Tyr Ser Gln Tyr Arg Pro Gln Val Val Ala Val Ile Gly Pro  
130 135 140

Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser Tyr Phe  
145 150 155 160

Leu Val Pro Gln Val Thr Tyr Ser Ala Ile Thr Asp Lys Leu Gln Asp  
165 170 175

Lys Arg Arg Phe Pro Ala Met Leu Arg Thr Val Pro Ser Ala Thr His  
180 185 190

His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp  
195 200 205

Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His  
210 215 220

Leu Leu Ser Gln Arg Leu Thr Asn Thr Gly Asp Ile Cys Ile Ala Phe  
225 230 235 240

Gln Glu Val Leu Pro Val Pro Glu Pro Asn Gln Ala Val Arg Pro Glu  
 245 250 255  
 Glu Gln Asp Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser  
 260 265 270  
 Ala Arg Val Val Val Ile Phe Ser Pro Glu Leu Ser Leu His Asn Phe  
 275 280 285  
 Phe Arg Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala  
 290 295 300  
 Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu  
 305 310 315 320  
 Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile  
 325 330 335  
 Pro Gly Phe Ser Gln Phe Arg Val Arg His Asp Lys Pro Gly Tyr Arg  
 340 345 350  
 Met Pro Asn Glu Thr Ser Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp  
 355 360 365  
 Ala Cys Met Asn Ile Thr Glu Ser Phe Asn Asn Val Leu Met Leu Ser  
 370 375 380  
 Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala  
 385 390 395 400  
 His Thr Leu His Arg Leu Leu His Cys Asn Gln Val Arg Cys Thr Lys  
 405 410 415  
 Gln Ile Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn  
 420 425 430  
 Phe Thr Leu Leu Gly Asn Gln Leu Phe Phe Asp Glu Gln Gly Asp Met  
 435 440 445  
 Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Gly Leu Ser Gln Asn  
 450 455 460  
 Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Glu Thr Arg Leu Thr  
 465 470 475 480  
 Tyr Ile Ser Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Ile  
 485 490 495  
 Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Pro Ile  
 500 505 510  
 Gly Leu His Pro Cys Cys Phe Glu Cys Val Asp Cys Pro Pro Asp Thr  
 515 520 525  
 Tyr Leu Asn Arg Ser Val Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly  
 530 535 540  
 Ser Met Trp Ser Tyr Lys Asn Asn Ile Ala Cys Phe Lys Arg Arg Leu  
 545 550 555 560



Ala Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Thr Ile Leu  
 565 570 575  
 Ala Ala Leu Gly Phe Ile Ser Thr Leu Ala Ile Leu Leu Ile Phe Trp  
 580 585 590  
 Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys  
 595 600 605  
 Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val  
 610 615 620  
 Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe  
 625 630 635 640  
 Phe Thr Val Cys Phe Ser Val Cys Leu Ser Cys Ile Thr Val Arg Ser  
 645 650 655  
 Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala  
 660 665 670  
 Tyr Gly Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe  
 675 680 685  
 Ile Thr Ala Val Lys Val Ala Leu Val Ala Gly Asn Met Leu Ala Thr  
 690 695 700  
 Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Ile  
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 Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr  
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 Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Val  
 740 745 750  
 Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu  
 755 760 765  
 Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met  
 770 775 780  
 Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr  
 785 790 795 800  
 Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys  
 805 810 815  
 Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn  
 820 825 830  
 Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser  
 835 840

<210> 9

<211> 838

<212> PRT

<213> Homo sapiens

<220>

<223> human T1R2 sweet taste receptor

<400> 9

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Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp
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Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp
      20             25             30

Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
      35             40             45

Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val
      50             55             60

Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu
      65             70             75             80

Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr
      85             90             95

Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu
      100            105            110

Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr
      115            120            125

Ser Asn Tyr Ile Ser Arg Val Val Ala Val Ile Gly Pro Asp Asn Ser
      130            135            140

Glu Ser Val Met Thr Val Ala Asn Phe Leu Ser Leu Phe Leu Leu Pro
      145            150            155            160

Gln Ile Thr Tyr Ser Ala Ile Ser Asp Glu Leu Arg Asp Lys Val Arg
      165            170            175

Phe Pro Ala Leu Leu Arg Thr Thr Pro Ser Ala Asp His His Val Glu
      180            185            190

Ala Met Val Gln Leu Met Leu His Phe Arg Trp Asn Trp Ile Ile Val
      195            200            205

Leu Val Ser Ser Asp Thr Tyr Gly Arg Asp Asn Gly Gln Leu Leu Gly
      210            215            220

Glu Arg Val Ala Arg Arg Asp Ile Cys Ile Ala Phe Gln Glu Thr Leu
      225            230            235            240

Pro Thr Leu Gln Pro Asn Gln Asn Met Thr Ser Glu Glu Arg Gln Arg
      245            250            255

Leu Val Thr Ile Val Asp Lys Leu Gln Gln Ser Thr Ala Arg Val Val
      260            265            270

Val Val Phe Ser Pro Asp Leu Thr Leu Tyr His Phe Phe Asn Glu Val
      275            280            285

Leu Arg Gln Asn Phe Thr Gly Ala Val Trp Ile Ala Ser Glu Ser Trp
      290            295            300
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Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu Gly His Leu Gly  
 305 310 315 320  
 Thr Phe Leu Gly Ile Thr Ile Gln Ser Val Pro Ile Pro Gly Phe Ser  
 325 330 335  
 Glu Phe Arg Glu Trp Gly Pro Gln Ala Gly Pro Pro Pro Leu Ser Arg  
 340 345 350  
 Thr Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn  
 355 360 365  
 Ala Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val  
 370 375 380  
 Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His  
 385 390 395 400  
 Ser Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr  
 405 410 415  
 Pro Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu  
 420 425 430  
 Asp His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu  
 435 440 445  
 Glu Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser  
 450 455 460  
 Val Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Gln Asp  
 465 470 475 480  
 Ile Ser Trp His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser  
 485 490 495  
 Lys Arg Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val  
 500 505 510  
 Cys Cys Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His  
 515 520 525  
 Thr Glu Asp Glu Tyr Glu Cys Gln Ala Cys Pro Asn Asn Glu Trp Ser  
 530 535 540  
 Tyr Gln Ser Glu Thr Ser Cys Phe Lys Arg Gln Leu Val Phe Leu Glu  
 545 550 555 560  
 Trp His Glu Ala Pro Thr Ile Ala Val Ala Leu Leu Ala Ala Leu Gly  
 565 570 575  
 Phe Leu Ser Thr Leu Ala Ile Leu Val Ile Phe Trp Arg His Phe Gln  
 580 585 590  
 Thr Pro Ile Val Arg Ser Ala Gly Gly Pro Met Cys Phe Leu Met Leu  
 595 600 605  
 Thr Leu Leu Leu Val Ala Tyr Met Val Val Pro Val Tyr Val Gly Pro  
 610 615 620

Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys  
 625 630 635 640  
 Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val  
 645 650 655  
 Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp  
 660 665 670  
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu  
 675 680 685  
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Arg Pro Gln Ser His  
 690 695 700  
 Pro Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys Asn  
 705 710 715 720  
 Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu Leu  
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 Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu Pro  
 740 745 750  
 Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe Tyr  
 755 760 765  
 Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser Gly  
 770 775 780  
 Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu Leu  
 785 790 795 800  
 Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu Phe  
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 Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln Gly  
 820 825 830  
 Tyr Thr Met Arg Arg Asp  
 835

<210> 10

<211> 2993

<212> DNA

<213> Rattus sp.

<220>

<223> rat T1R2 sweet taste receptor

<400> 10

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<212> DNA

<213> Homo sapiens

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<223> human T1R2 sweet taste receptor

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 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human T1R3 sweet taste receptor

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 Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu  
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 Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg  
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 Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val  
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 Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly  
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 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro  
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 Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr  
 115 120 125  
 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro  
 130 135 140  
 His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe  
 145 150 155 160  
 Leu Met Pro Gln Val Ser Tyr Gly Ala Ser Met Glu Leu Leu Ser Ala  
 165 170 175  
 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val  
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Ile	Phe	Ser	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu		
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Gln	Asp	Val	Leu	His	Gln	Val	Asn	Gln	Ser	Ser	Val	Gln	Val	Val	Leu		
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Leu	Phe	Ala	Ser	Val	His	Ala	Ala	His	Ala	Leu	Phe	Asn	Tyr	Ser	Ile		
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Ser	Ser	Arg	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Leu		
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Arg	Cys	Pro	Gln	Cys	Asp	Cys	Ile	Thr	Leu	Gln	Asn	Val	Ser	Ala	Gly		
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 His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr  
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 Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg  
 740 745 750  
 Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met  
 755 760 765  
 Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn  
 770 775 780  
 Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu  
 785 790 795 800  
 Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu  
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Gly Lys His Glu  
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<210> 16  
<211> 3240  
<212> DNA  
<213> Mus musculus

<220>  
<223> mouse Sac non taster 129 T1R3 sweet taste receptor  
genomic

<400> 16  
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<210> 17

<211> 2577

<212> DNA

<213> Mus musculus

<220>

<223> mouse Sac non taster 129 T1R3 sweet taste receptor  
CDS

<400> 17

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<220>  
 <223> mouse Sac non taster 129 T1R3 sweet taste receptor

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 Ala Thr Leu Asn Gln Arg Ala Gln Pro Asn Ser Thr Leu Cys Asn Arg  
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 Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly  
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 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser  
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 Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr  
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 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro  
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 His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe  
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 Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp  
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 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val  
 180 185 190  
 Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp  
 195 200 205  
 Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser  
 210 215 220  
 Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu  
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Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	Gln	Ser	Lys	Met	Tyr	Trp	Pro	Gly	
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Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	
			500					505					510			
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	
			515				520					525				
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	
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Pro	Cys	Asn	Gln	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Ala	Cys	Leu	
545					550					555					560	

Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser  
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 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu Ala Ala Leu  
                     580                    585                    590  
 Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln Ala Ser Gly  
                     595                    600                    605  
 Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu  
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 Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala  
                     625                    630                    635                    640  
 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu  
                     645                    650                    655  
 Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser  
                     660                    665                    670  
 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu  
                     675                    680                    685  
 Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr  
                     690                    695                    700  
 Leu Thr Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro  
                     705                    710                    715                    720  
 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly  
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 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly  
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 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly  
                     755                    760                    765  
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val  
                     770                    775                    780  
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met  
                     785                    790                    795                    800  
 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu  
                     805                    810                    815  
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu  
                     820                    825                    830  
 Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly  
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 Gly Gly Glu Ala Ala Gln Glu His Asn Glu  
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<210> 19  
 <211> 2577  
 <212> DNA  
 <213> Mus musculus

<220>  
 <223> mouse Sac taster SWR T1R3 sweet taste receptor CDS

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<210> 20  
 <211> 858  
 <212> PRT  
 <213> Mus musculus

<220>  
 <223> mouse Sac taster SWR T1R3 sweet taste receptor

<400> 20

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Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu  
35 40 45  
Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Ser Ile Leu Cys Asn Arg  
50 55 60  
Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val  
65 70 75 80  
Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly  
85 90 95  
Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser  
100 105 110  
Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr  
115 120 125  
Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro  
130 135 140  
His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe  
145 150 155 160  
Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp  
165 170 175  
Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val  
180 185 190  
Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp  
195 200 205  
Val Ala Ala Leu Gly Ser Asp Asp Tyr Gly Arg Glu Gly Leu Ser  
210 215 220  
Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu  
225 230 235 240  
Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val  
245 250 255  
Leu Asp Val Leu Cys Gln Val Asn Gln Ser Lys Val Gln Val Val Val  
260 265 270  
Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile  
275 280 285  
His His Gly Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu  
290 295 300  
Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr  
305 310 315 320

Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His  
325 330 335  
Tyr Val Glu Thr His Leu Ala Leu Ala Ala Asp Pro Ala Phe Cys Ala  
340 345 350  
Ser Leu Asn Ala Glu Leu Asp Leu Glu Glu His Val Met Gly Gln Arg  
355 360 365  
Cys Pro Gln Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu  
370 375 380  
Leu Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr  
385 390 395 400  
Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln  
405 410 415  
Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln  
420 425 430  
Leu Leu Glu Asn Met Tyr Asn Met Ser Phe His Ala Arg Asp Leu Thr  
435 440 445  
Leu Gln Phe Asp Ala Glu Gly Asn Val Asp Met Glu Tyr Asp Leu Lys  
450 455 460  
Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr  
465 470 475 480  
Phe Asn Gly Thr Leu Gln Leu Gln Gln Ser Lys Met Tyr Trp Pro Gly  
485 490 495  
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500 505 510  
Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp  
515 520 525  
Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr  
530 535 540  
Pro Cys Asn Gln Asp Gln Trp Ser Pro Glu Lys Ser Thr Ala Cys Leu  
545 550 555 560  
Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser  
565 570 575  
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Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu  
610 615 620  
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625 630 635 640

Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu  
 645 650 655  
 Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser  
 660 665 670  
 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu  
 675 680 685  
 Val Val Leu Ser Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr  
 690 695 700  
 Leu Thr Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro  
 705 710 715 720  
 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly  
 725 730 735  
 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly  
 740 745 750  
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly  
 755 760 765  
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val  
 770 775 780  
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met  
 785 790 795 800  
 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu  
 805 810 815  
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu  
 820 825 830  
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<210> 21

<211> 3200

<212> DNA

<213> Mus musculus

<220>

<223> mouse Sac taster C57 T1R3 sweet taste receptor  
genomic

<400> 21

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<210> 22

<211> 2577

<212> DNA

<213> Mus musculus

<220>

<223> mouse Sac taster C57 T1R3 sweet taste receptor CDS

<400> 22

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ggccgctaca	accgtgccc	tggtctcacc	ttcgccatgc	tagcttattt	catcacctgg	2340
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ggtgctatcc	tagtctgtgc	cctgggcac	ctggtcacct	tccacctgcc	caagtgtctat	2460
gtgcttcttt	ggctgccaaa	gctcaacacc	caggagtctt	tcctgggaag	gaatgccaa	2520
aaagcagcag	atgagaacag	tggcgggtgt	gaggcagctc	aggacacaa	tgaatga	2577

<210> 23

<211> 858

<212> PRT

<213> Mus musculus

<220>

<223> mouse Sac taster C57 T1R3 sweet taste receptor

<400> 23

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Leu	Gly	Met	Gly	Ala	Ser	Leu	Cys	Leu	Ser	Gln	Gln	Phe	Lys	Ala	Gln
			20						25				30		

Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Ser	Thr	Glu	Glu
		35					40					45			

Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Ser	Ile	Pro	Cys	Asn	Arg
	50						55				60				

Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val	
65					70					75					80	
Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly	
			85						90					95		
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Ser	
		100						105					110			
Ser	Leu	Met	Phe	Leu	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr	
		115					120					125				
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro	
	130					135					140					
His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe	
145					150					155					160	
Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp	
			165						170					175		
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val	
			180					185					190			
Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp	
	195						200					205				
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser	
	210					215					220					
Ile	Phe	Ser	Ser	Leu	Ala	Asn	Ala	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu	
225					230					235					240	
Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val	
				245					250					255		
Leu	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val	
		260						265					270			
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile	
		275					280					285				
His	His	Gly	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu	
	290					295					300					
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr	
305					310					315					320	
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His	
			325						330					335		
Tyr	Val	Glu	Thr	His	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Ala	Phe	Cys	Ala	
			340					345					350			
Ser	Leu	Asn	Ala	Glu	Leu	Asp	Leu	Glu	Glu	His	Val	Met	Gly	Gln	Arg	
		355					360					365				
Cys	Pro	Arg	Cys	Asp	Asp	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu	
	370					375					380					

Leu Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr  
 385 390 395 400  
 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln  
 405 410 415  
 Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln  
 420 425 430  
 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe His Ala Arg Asp Leu Thr  
 435 440 445  
 Leu Gln Phe Asp Ala Glu Gly Asn Val Asp Met Glu Tyr Asp Leu Lys  
 450 455 460  
 Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr  
 465 470 475 480  
 Phe Asn Gly Thr Leu Gln Leu Gln Gln Ser Lys Met Tyr Trp Pro Gly  
 485 490 495  
 Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln  
 500 505 510  
 Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp  
 515 520 525  
 Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr  
 530 535 540  
 Pro Cys Asn Gln Asp Gln Trp Ser Pro Glu Lys Ser Thr Ala Cys Leu  
 545 550 555 560  
 Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser  
 565 570 575  
 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu Ala Leu  
 580 585 590  
 Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln Ala Ser Gly  
 595 600 605  
 Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu  
 610 615 620  
 Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala  
 625 630 635 640  
 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu  
 645 650 655  
 Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser  
 660 665 670  
 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu  
 675 680 685  
 Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr  
 690 695 700



Leu Ile Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro  
 705 710 715 720  
 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly  
 725 730 735  
 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly  
 740 745 750  
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly  
 755 760 765  
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val  
 770 775 780  
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met  
 785 790 795 800  
 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu  
 805 810 815  
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu  
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 <212> DNA  
 <213> Rattus sp.

<220>  
 <223> rat T1R3 sweet taste receptor CDS

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<210> 25  
 <211> 858  
 <212> PRT  
 <213> Rattus sp.

<220>  
 <223> rat T1R3 sweet taste receptor

<400> 25  
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 20 25 30  
 Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Thr Thr Glu Glu  
 35 40 45  
 Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Gly Ile Leu Cys Thr Arg  
 50 55 60  
 Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val  
 65 70 75 80  
 Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly  
 85 90 95  
 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Pro  
 100 105 110  
 Ser Leu Met Phe Met Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr  
 115 120 125  
 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro  
 130 135 140

His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe  
 145 150 155 160  
 Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp  
 165 170 175  
 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val  
 180 185 190  
 Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp  
 195 200 205  
 Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser  
 210 215 220  
 Ile Phe Ser Gly Leu Ala Asn Ser Arg Gly Ile Cys Ile Ala His Glu  
 225 230 235 240  
 Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val  
 245 250 255  
 Val Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val  
 260 265 270  
 Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile  
 275 280 285  
 Leu His Asp Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu  
 290 295 300  
 Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr  
 305 310 315 320  
 Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His  
 325 330 335  
 Tyr Val Glu Thr Arg Leu Ala Leu Ala Ala Asp Pro Thr Phe Cys Ala  
 340 345 350  
 Ser Leu Lys Ala Glu Leu Asp Leu Glu Glu Arg Val Met Gly Pro Arg  
 355 360 365  
 Cys Ser Gln Cys Asp Tyr Ile Met Leu Gln Asn Leu Ser Ser Gly Leu  
 370 375 380  
 Met Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr  
 385 390 395 400  
 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln  
 405 410 415  
 Cys Asn Val Ser His Cys His Thr Ser Glu Pro Val Gln Pro Trp Gln  
 420 425 430  
 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe Arg Ala Arg Asp Leu Thr  
 435 440 445  
 Leu Gln Phe Asp Ala Lys Gly Ser Val Asp Met Glu Tyr Asp Leu Lys  
 450 455 460

Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr	
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Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	His	Ser	Lys	Met	Tyr	Trp	Pro	Gly	
				485					490					495		
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln	
			500					505					510			
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp	
			515				520					525				
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr	
	530					535					540					
Pro	Cys	Gly	Lys	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Thr	Cys	Leu	
545					550					555					560	
Pro	Arg	Arg	Pro	Lys	Phe	Leu	Ala	Trp	Gly	Glu	Pro	Ala	Val	Leu	Ser	
				565					570					575		
Leu	Leu	Leu	Leu	Leu	Cys	Leu	Val	Leu	Gly	Leu	Thr	Leu	Ala	Ala	Leu	
			580					585					590			
Gly	Leu	Phe	Val	His	Tyr	Trp	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly	
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Gly	Ser	Leu	Phe	Cys	Phe	Gly	Leu	Ile	Cys	Leu	Gly	Leu	Phe	Cys	Leu	
	610					615					620					
Ser	Val	Leu	Leu	Phe	Pro	Gly	Arg	Pro	Arg	Ser	Ala	Ser	Cys	Leu	Ala	
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Gln	Gln	Pro	Met	Ala	His	Leu	Pro	Leu	Thr	Gly	Cys	Leu	Ser	Thr	Leu	
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Phe	Leu	Gln	Ala	Ala	Glu	Ile	Phe	Val	Glu	Ser	Glu	Leu	Pro	Leu	Ser	
			660					665					670			
Trp	Ala	Asn	Trp	Leu	Cys	Ser	Tyr	Leu	Arg	Gly	Pro	Trp	Ala	Trp	Leu	
		675					680					685				
Val	Val	Leu	Leu	Ala	Thr	Leu	Val	Glu	Ala	Ala	Leu	Cys	Ala	Trp	Tyr	
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Leu	Met	Ala	Phe	Pro	Pro	Glu	Val	Val	Thr	Asp	Trp	Gln	Val	Leu	Pro	
705					710					715					720	
Thr	Glu	Val	Leu	Glu	His	Cys	Arg	Met	Arg	Ser	Trp	Val	Ser	Leu	Gly	
				725					730					735		
Leu	Val	His	Ile	Thr	Asn	Ala	Val	Leu	Ala	Phe	Leu	Cys	Phe	Leu	Gly	
			740					745					750			
Thr	Phe	Leu	Val	Gln	Ser	Gln	Pro	Gly	Arg	Tyr	Asn	Arg	Ala	Arg	Gly	
		755					760					765				
Leu	Thr	Phe	Ala	Met	Leu	Ala	Tyr	Phe	Ile	Ile	Trp	Val	Ser	Phe	Val	
						775					780					

Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met  
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 Gly Ala Ile Leu Phe Cys Ala Leu Gly Ile Leu Ala Thr Phe His Leu  
 805 810 815  
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Glu Leu Asn Thr Gln Glu  
 820 825 830  
 Phe Phe Leu Gly Arg Ser Pro Lys Glu Ala Ser Asp Gly Asn Ser Gly  
 835 840 845  
 Ser Ser Glu Ala Thr Arg Gly His Ser Glu  
 850 855